#10

FIG. 1


```
ATATTGCTGAGCTCAGGGAGTGAGGGCCCCACATTTGAGACAGTGAGCCCCAAGAAGAGG      60
GATCCCTGCTCCAGCAGCTGCAAGGTGCAAGAAGAAGAAGATCCCAGGGAGGAAAATGTG     120
                                                    M  C            2
CTGGAGACCCCTGTGTCGGTTCCTGTGGCTTTGGTCCTATCTGTCTTATGTTCAAGCAGT     180
 W  R  P  L  C  R  F  L  W  L  W  S  Y  L  S  Y  V  Q  A  V      22
GCCTATCCAGAAAGTCCAGGATGACACCAAAACCCTCATCAAGACCATTGTCACCAGGAT     240
 P  I  Q  K  V  Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I      42
CAATGACATTTCACACACGCAGTCGGTATCCGCCAAGCAGAGGGTCACTGGCTTGGACTT     300
 N  D  I  S  H  T  Q  S  V  S  A  K  Q  R  V  T  G  L  D  F      62
CATTCCTGGGCTTCACCCCATTCTGAGTTTGTCCAAGATGGACCAGACTCTGGCAGTCTA     360
 I  P  G  L  H  P  I  L  S  L  S  K  M  D  Q  T  L  A  V  Y      82
TCAACAGGTCCTCACCAGCCTGCCTTCCCAAAATGTGCTGCAGATAGCCAATGACCTGGA     420
 Q  Q  V  L  T  S  L  P  S  Q  N  V  L  Q  I  A  N  D  L  E     102
GAATCTCCGAGACCTCCTCCATCTGCTGGCCTTCTCCAAGAGCTGCTCCCTGCCTCAGAC     480
 N  L  R  D  L  L  H  L  L  A  F  S  K  S  C  S  L  P  Q  T     122
CAGTGGCCTGCAGAAGCCAGAGAGCCTGGATGGCGTCCTGGAAGCCTCACTCTACTCCAC     540
 S  G  L  Q  K  P  E  S  L  D  G  V  L  E  A  S  L  Y  S  T     142
AGAGGTGGTGGCTTTGAGCAGGCTGCAGGGCTCTCTGCAGGACATTCTTCAACAGTTGGA     600
 E  V  V  A  L  S  R  L  Q  G  S  L  Q  D  I  L  Q  Q  L  D     162
TGTTAGCCCTGAATGCTGAAGTTTCAAAGGCCACCAGGCTCCCAAGAATCATGTAGAGGG     660
 V  S  P  E  C  *                                              167
AAGAAACCTTGGCTTCCAGGGGTCTTCAGGAGAAGAGAGCCATGTGCACACATCCATCAT     720
TCATTTCTCTCCCTCCTGTAGACCACCCATCCAAAGGCATGACTCCACAATGCTTGACTC     780
AAGTTATCCACACAACTTCATGAGCACAAGGAGGGGCCAGCCTGCAGAGGGGACTCTCAC     840
CTAGTTCTTCAGCAAGTAGAGATAAGAGCCATCCCATCCCCTCCATGTCCCACCTGCTCC     900
GGGTACATGTTCCTCCGTGGGTACACGCTTCGCTGCGGCCCAGGAGAGGTGAGGTAGGGA     960
TGGGTAGAGCCTTTGGGCTGTCTCAGAGTCTTTGGGAGCACCGTGAAGGCTGCATCCACA    1020
CACAGCTGGAAACTCCCAAGCAGCACACGATGGAAGCACTTATTTATTTATTCTGCATTC    1080
TATTTTGGATGGATCTGAAGCAAGGCATCAGCTTTTTCAGGCTTTGGGGGTCAGCCAGGA    1140
TGAGGAAGGCTCCTGGGGTGCTGCTTTCAATCCTATTGATGGGTCTGCCCGAGGCAAACC    1200
TAATTTTTGAGTGACTGGAAGGAAGGTTGGGATCTTCCAAACAAGAGTCTATGCAGGTAG    1260
CGCTCAAGATTGACCTCTGGTGACTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAAC    1320
ACGTTTGCAGCGGCATTGCCGGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTT    1380
TGTCAAGTGTAATATGTATCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGT    1440
GAAGGATCCGGAAGTGTTCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGA    1500
GGCATTTTCTTACCTCTGTGGCCACATAGTGTGGCTTTGTGAAAAGGACAAAGGAGTTGA    1560
CTCTTTCCGGAACATTTGGAGTGTACCAGGCACCCTTGGAGGGGCTAAAGCTACAGGCCT    1620
TTTGTTGGCATATTGCTGAGCTCAGGGAGTGAGGGCCCCACATTTGAGACAGTGAGCCCC    1680
AAGAAAAGGGTCCCTGGTGTAGATCTCCAAGGTTGTCCAGGGTTGATCTCACAATGCGTT    1740
TCTTAAGCAGGTAGACGTTTGCATGCCAATATGTGGTTCTCATCTGATTGGTTCATCCAA    1800
AGTAGAACCCTGTCTCCCACCCATTCTGTGGGGAGTTTTGTTCCAGTGGGAATGAGAAAT    1860
CACTTAGCAGATGGTCCTGAGCCCTGGGCCAGCACTGCTGAGGAAGTGCCAGGGCCCCAG    1920
GCCAGGCTGCCAGAATTGCCCTTCGGGCTGGAGGATGAACAAAGGGGCTTGGGTTTTTCC    1980
ATCACCCCTGCACCCTATGTCACCATCAAACTGGGGGGCAGATCAGTGAGAGGACACTTG    2040
ATGGAAAGCAATACACTTTAAGACTGAGCACAGTTTCGTGCTCAGCTCTGTCTGGTGCTG    2100
TGAGCTAGAGAAGCTCACCACATACATATAAAAATCAGAGGCTCATGTCCCTGTGGTTAG    2160
ACCCTACTCGCGGCGGTGTACTCCACCACAGCAGCACCGCACCGCTGGAAGTACAGTGCT    2220
GTCTTCAACAGGTGTGAAAGAACCTGAGCTGAGGGTGACAGTGCCCAGGGGAACCCTGCT    2280
TGCAGTCTATTGCATTTACATACCGCATTTCAGGGCACATTAGCATCCACTCCTATGGTA    2340
GCACACTGTTGACAATAGGACAAGGGATAGGGGTTGACTATCCCTTATCCAAAATGCTTG    2400
GGACTAGAAGAGTTTTGGATTTTAGAGTCTTTTCAGGCATAGGTATATTTGAGTATATAT    2460
AAAATGAGATATCTTGGGGATGGGGCCCAAGTATAAACATGAAGTTCATTTATATTTCAT    2520
AATACCGTATAGACACTGCTTGAAGTGTAGTTTTATACAGTGTTTTAAATAACGTTGTAT    2580
GCATGAAAGACGTTTTTACAGCATGAACCTGTCTACTCATGCCAGCACTCAAAAACCTTG    2640
GGGTTTTGGAGCAGTTTGGATCTTGGGTTTTCTGTTAAGAGATGGTTAGCTTATACCTAA    2700
AACCATAATGGCAAACAGGCTGCAGGACCAGACTGGATCCTCAGCCCTGAAGTGTGCCCT    2760
TCCAGCCAGGTCATACCCTGTGGAGGTGAGCGGGATCAGGTTTTGTGGTGCTAAGAGAGG    2820
AGTTGGAGGTAGATTTTGGAGGATCTGAGGGC                                 2852
```

FIG.2

```
---G--GTTG CAAGGCCCAA GAAGCCCA-- -TCCTGGGAA GGAAAATGCA      50
TTGGGGAACC CTGTG-CGGA TTCTTGTGGC TTTGGCCCTA TCTTTTCTAT     100
GTCCAAGCTG TGCCCATCCA AAAAGTCCAA GATGACACCA AAACCCTCAT     150
CAAGACAATT GTCACCAGGA TCAATGACAT TTCACACACG CAGTCAGTCT     200
CCTCCAAACA GAAAGTCACC GGTTTGGACT TCATTCCTGG GCTCCACCCC     250
ATCCTGACCT TATCCAAGAT GGACCAGACA CTGGCAGTCT ACCAACAGAT     300
CCTCACCAGT ATGCCTTCCA GAAACGTGAT CCAAATATCC AACGACCTGG     350
AGAACCTCCG GGATCTTCTT CACGTGCTGG CCTTCTCTAA GAGCTGCCAC     400
TTGCCCTGGG CCAGTGGCCT GGAGACCTTG GACAGCCTGG GGGGTGTCCT     450
GGAAGCTTCA GGCTACTCCA CAGAGGTGGT GGCCCTGAGC AGGCTGCAGG     500
GGTCTCTGCA GGACATGCTG TGGCAGCTGG ACCTCAGCCC TGGGTGCTGA     550
GGCCTTGAAG GTCACTCTTC CTGCAAGGAC T-ACGTTAAG GGAAGGAACT     600
CTGGTTTCCA GGTATCTCCA GGATTGAAGA GCATTGCATG GACACCCCTT     650
ATCCAGGACT CTGTCAATTT CCCTGACTCC TCTAAGCCAC TCTTCCAAAG     700
G                                                         701
```

1	MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
16	LEU PHE TYR VAL GLN ALA↓VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR GLN SER VAL SER SER LYS GLN LYS VAL THR GLY LEU
61	ASP PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET
76	ASP GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO
91	SER ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG
106	ASP LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO
121	TRP ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU
136	GLU ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU
151	GLN GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO
166	GLY CYS END

FIG.3

```
MOUSE   MCWRPLCRFL WLWSYLSYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS   50
HUMAN   MHWGTLCGFL WLWPYLFYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS

MOUSE   VSAKQRVTGL DFIPGLHPIL SLSKMDQTLA VYQQVLTSLP SQNVLQIAND  100
HUMAN   VSSKQKVTGL DFIPGLHPIL TLSKMDQTLA VYQQILTSMP SRNVIQISND

MOUSE   LENLRDLLHL LAFSKSCSLP QTSGLQKPES LDGVLEASLY STEVVALSRL  150
HUMAN   LENLRDLLHV LAFSKSCHLP WASGLETLDS LGGVLEASGY STEVVALSRL

MOUSE   QGSLQDILQQ LDVSPEC                                      167
HUMAN   QGSLQDMLWQ LDLSPGC
```

FIG.4

1	MET CYS TRP ARG PRO LEU CYS ARG PHE LEU TRP LEU TRP SER TYR
16	LEU SER TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR SER VAL SER ALA LYS GLN ARG VAL THR GLY LEU ASP
61	PHE ILE PRO GLY LEU HIS PRO ILE LEU SER LEU SER LYS MET ASP
76	GLN THR LEU ALA VAL TYR GLN GLN VAL LEU THR SER LEU PRO SER
91	GLN ASN VAL LEU GLN ILE ALA ASN ASP LEU GLU ASN LEU ARG ASP
106	LEU LEU HIS LEU LEU ALA PHE SER LYS SER CYS SER LEU PRO GLN
121	THR SER GLY LEU GLN LYS PRO GLU SER LEU ASP GLY VAL LEU GLU
136	ALA SER LEU TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU GLN
151	GLY SER LEU GLN ASP ILE LEU GLN GLN LEU ASP VAL SER PRO GLU
166	CYS END

FIG.5

1	MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
16	LEU PHE TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR SER VAL SER SER LYS GLN LYS VAL THR GLY LEU ASP
61	PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET ASP
76	GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO SER
91	ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG ASP
106	LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO TRP
121	ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU GLU
136	ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU GLN
151	GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO GLY
166	CYS END

FIG.6

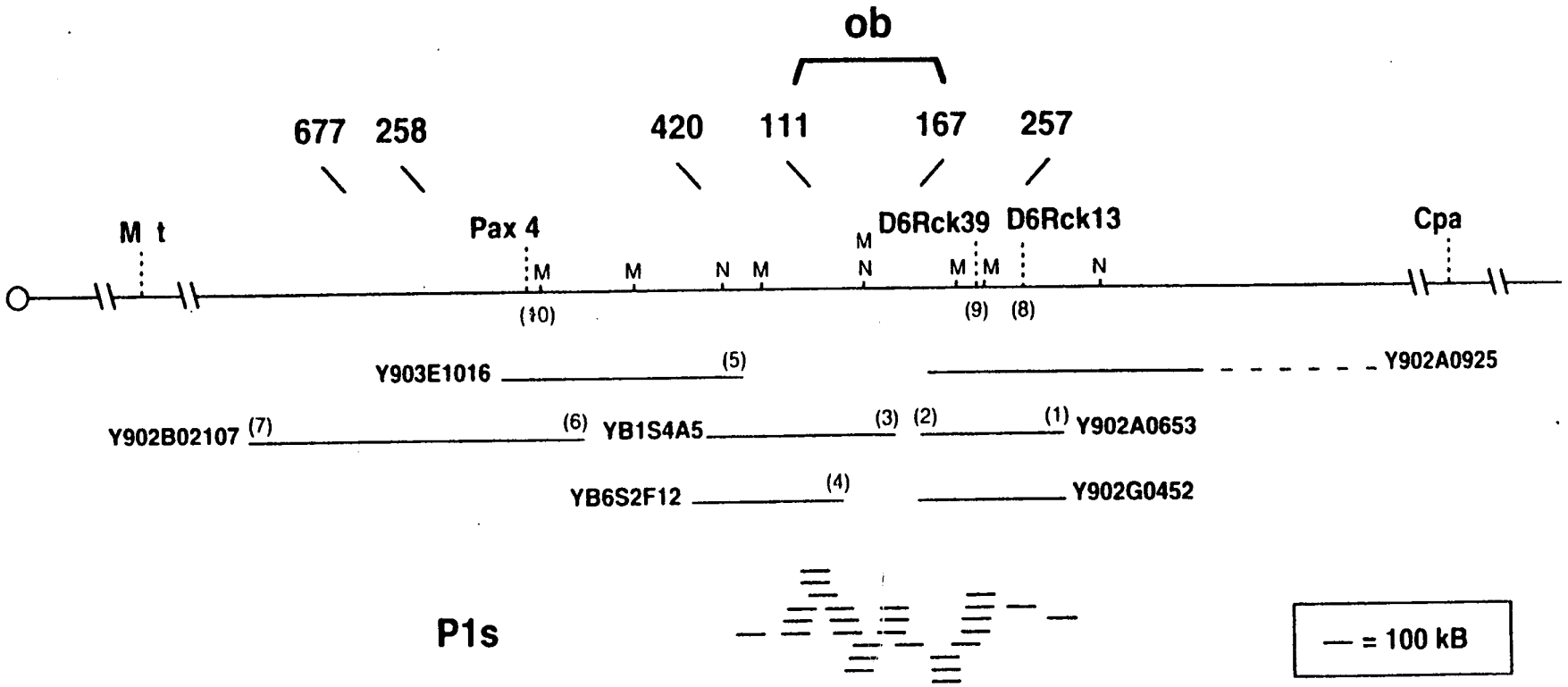


FIG.7

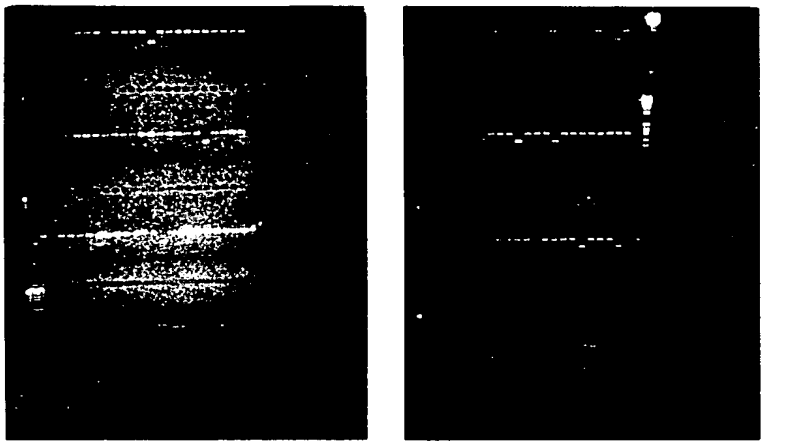


FIG.8

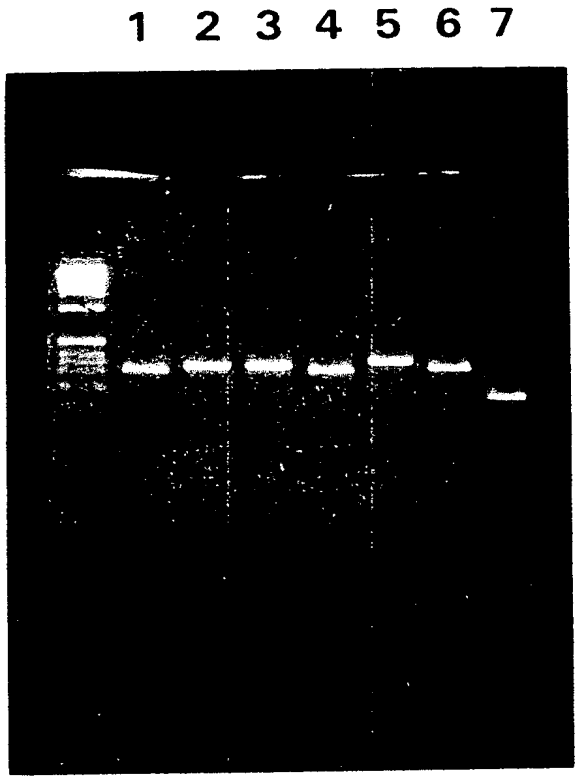


FIG.9

```
          +10         +20         +30         +40
GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG
---------- ---------- ---------- ---------- ----------
CACGTTCTTC TTCTTCTAGG GTCCCGTCCT TTTACACGAC CTCTGGGGAC

          +10         +20         +30         +40
TGTCGGGTCC NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC
---------- ?----?---- ---------- --------?- ----------
ACAGCCCAGG NCACCNAAAC CAGGATAGAC AGAATACANG TTCGTCACGG

          +10         +20         +30         +40
TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA
---------- ---------- ---------- ---------- ----------
ATAGGTCTTT CAGGTCCTAC TGTGGTTTTC GGAGTAGTTC TGGTAACAGT

          +10         +20         +30         +40
NCAGGATCAC TGANATTTCA CACACG
?--------- ---?------ ------
NGTCCTAGTG ACTNTAAAGT GTGTGC
```

FIG.10

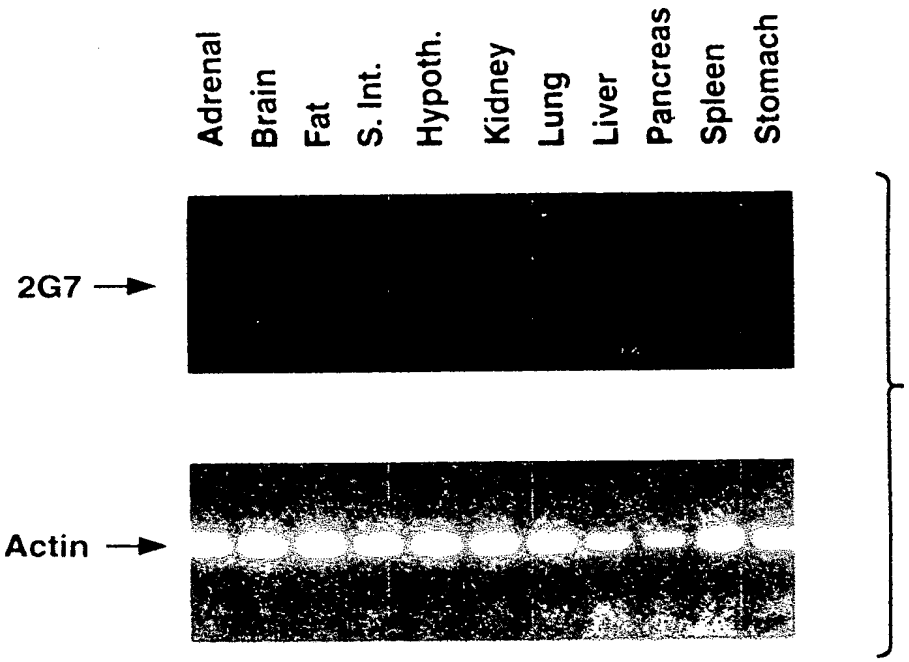


FIG. 11A

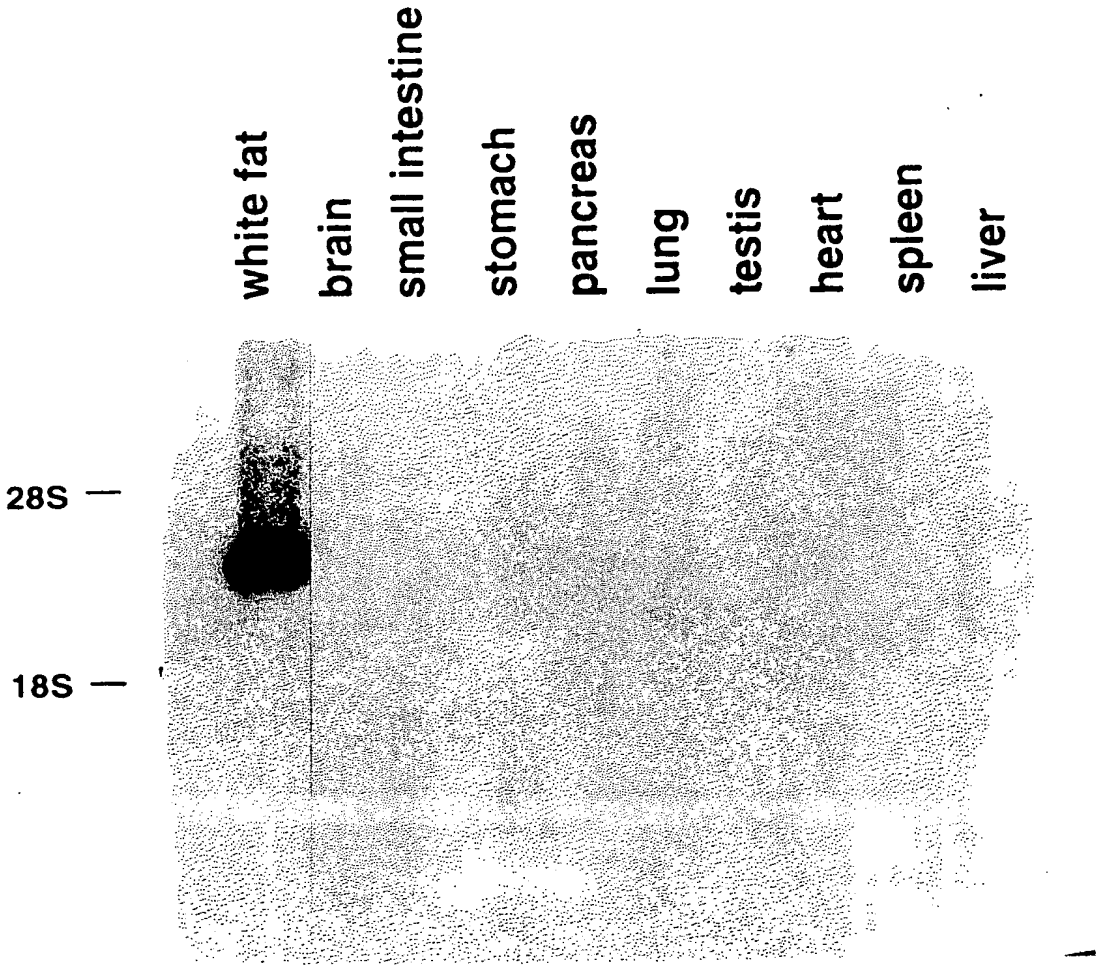


FIG.11B

FIG.12A

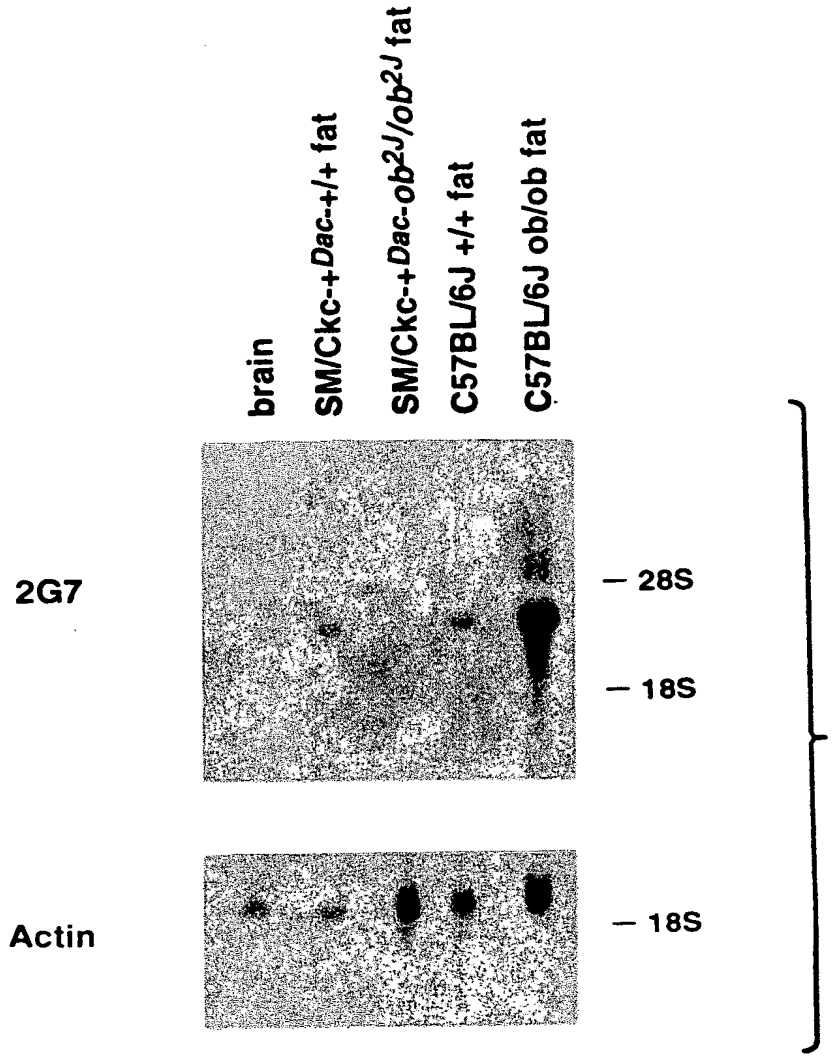


FIG.12B

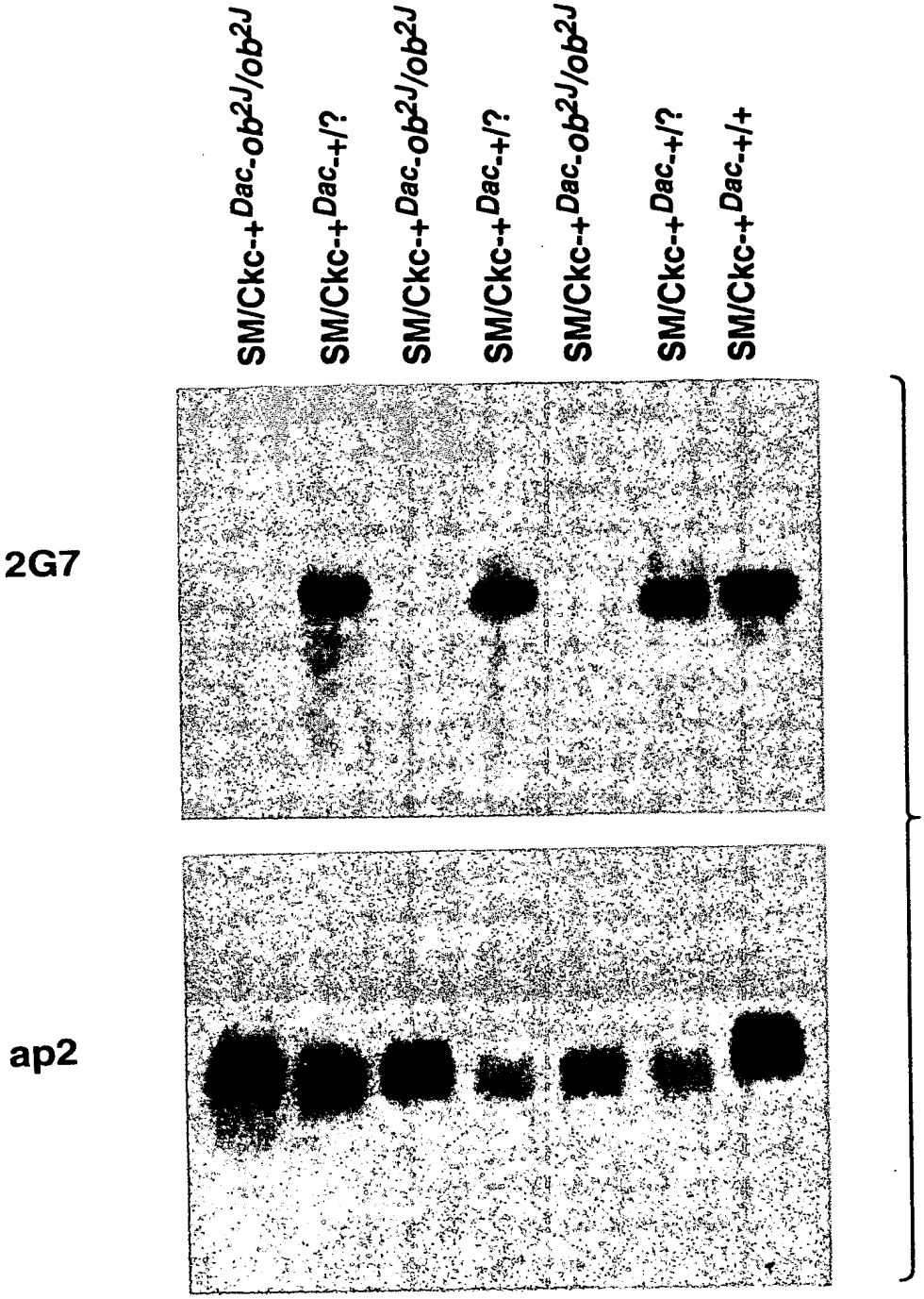


FIG.13

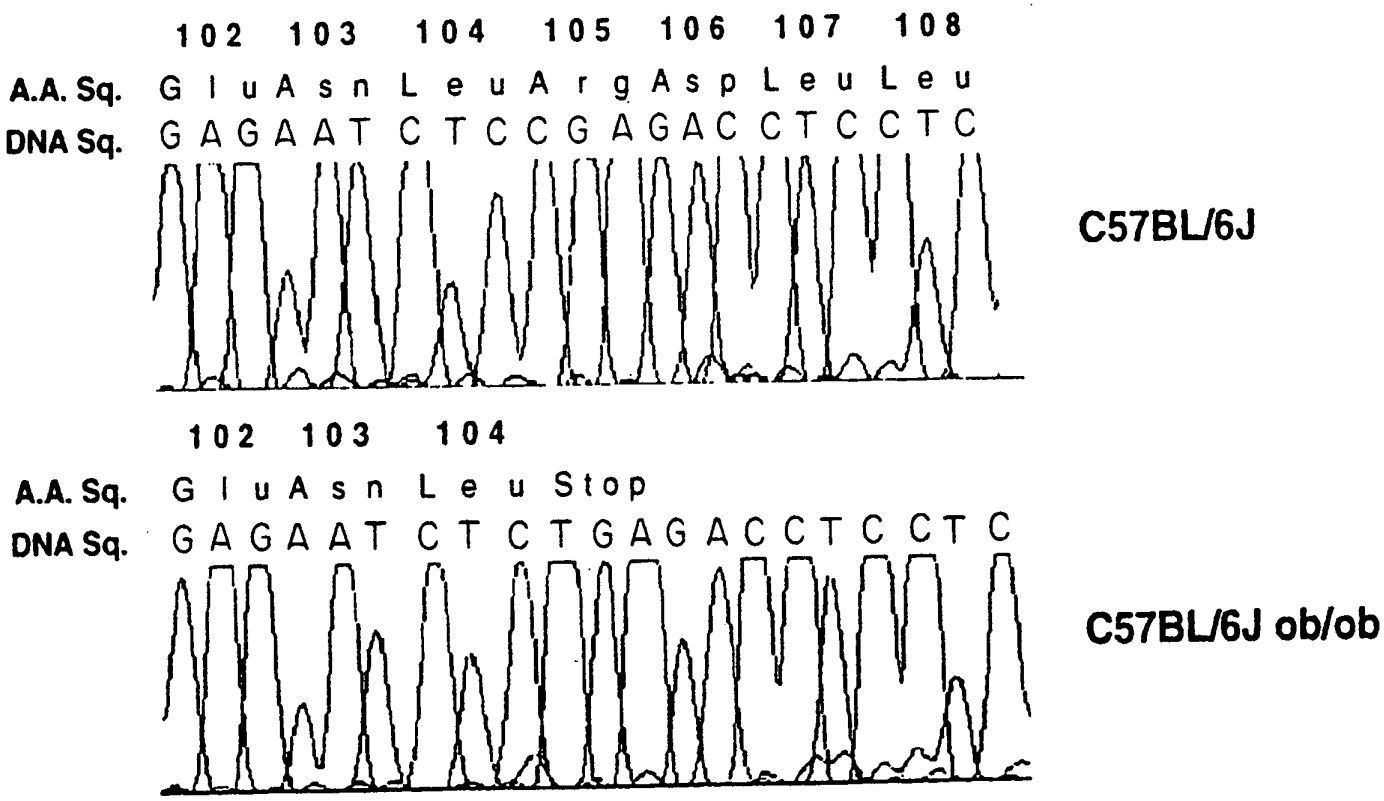


FIG.14

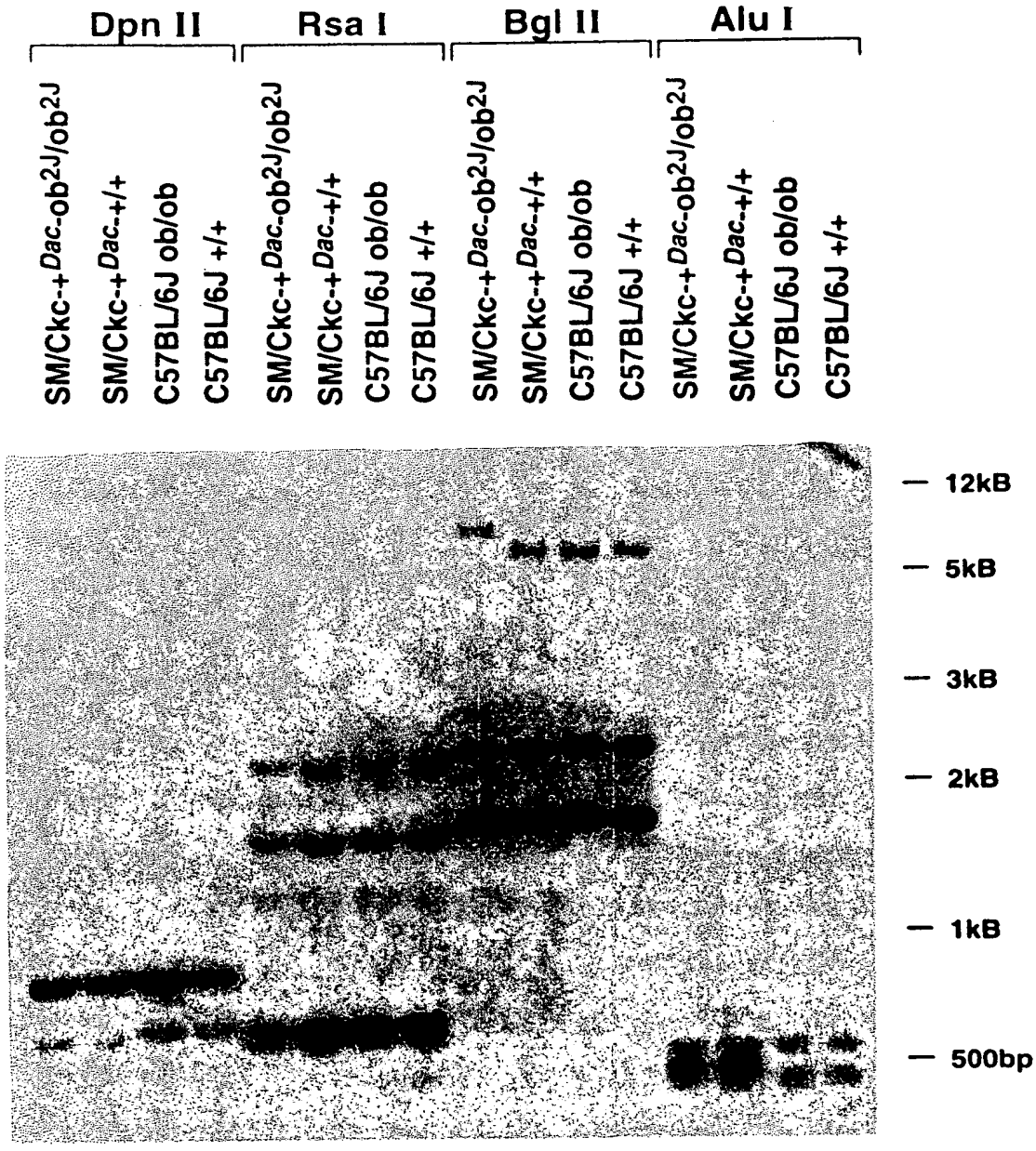


FIG.15A

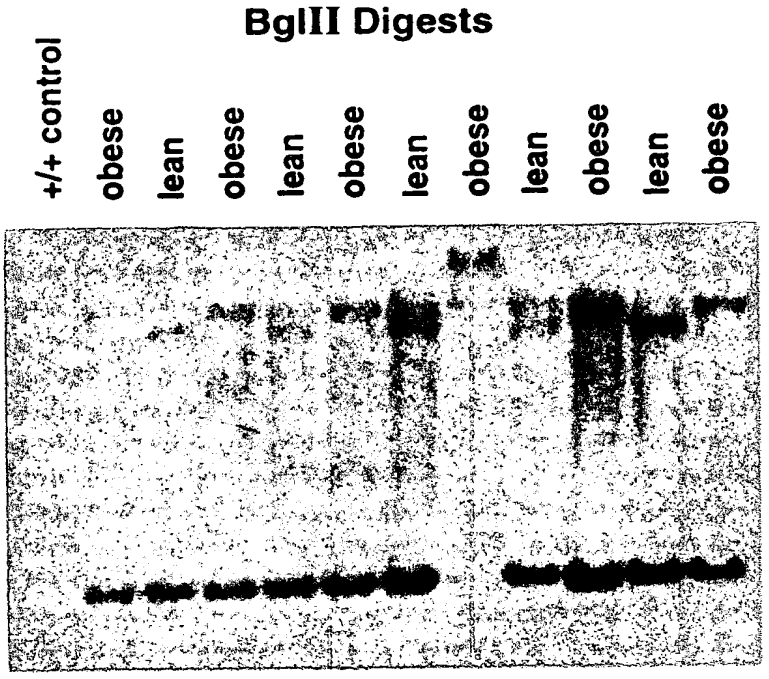


FIG.15B

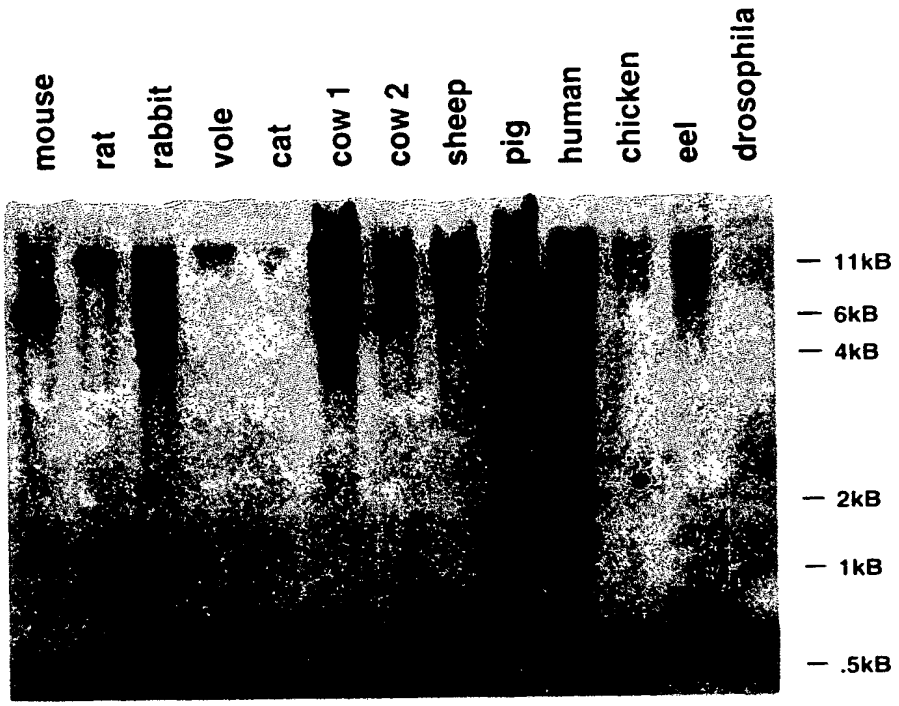


FIG.16

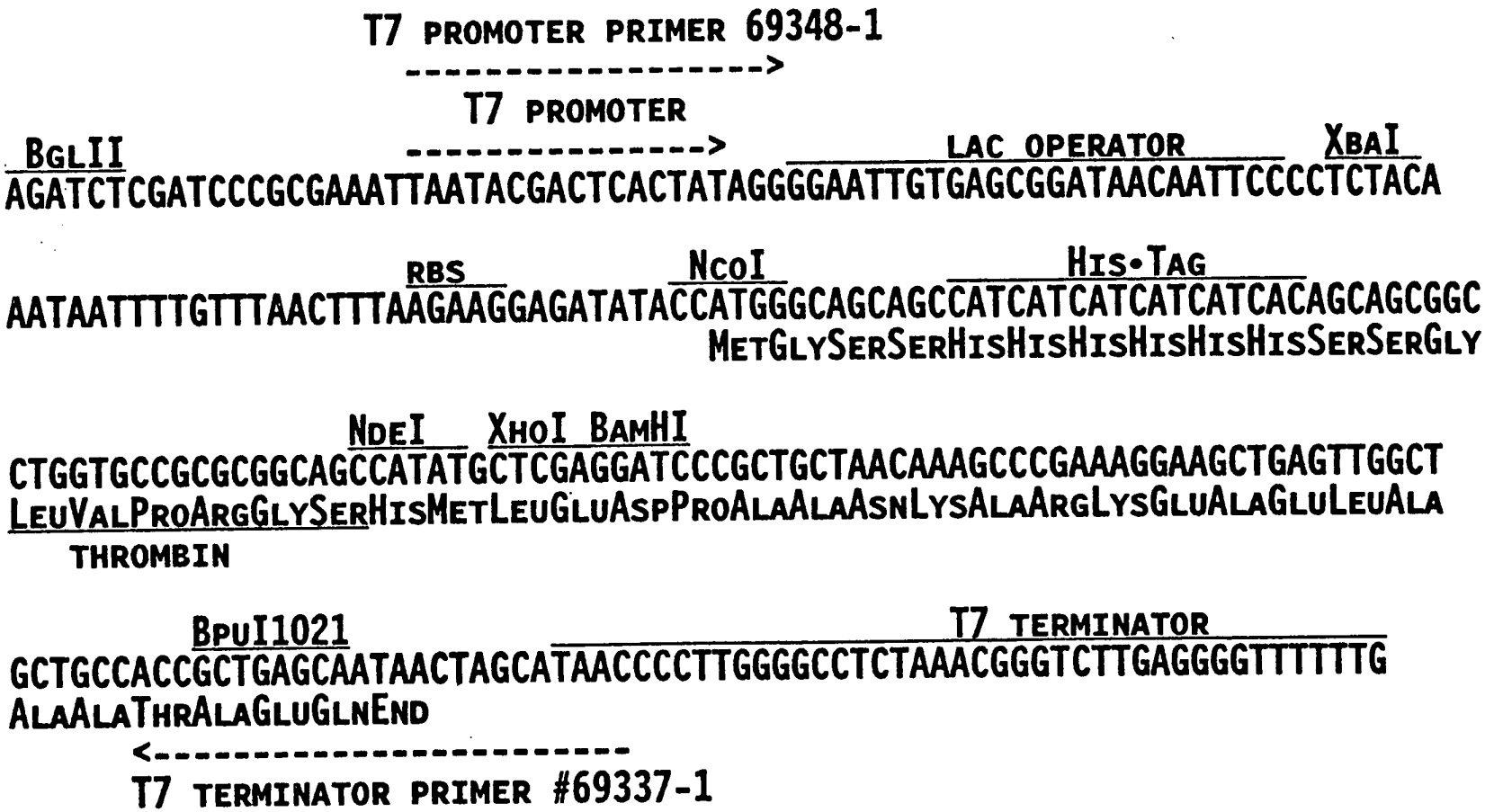


FIG.17

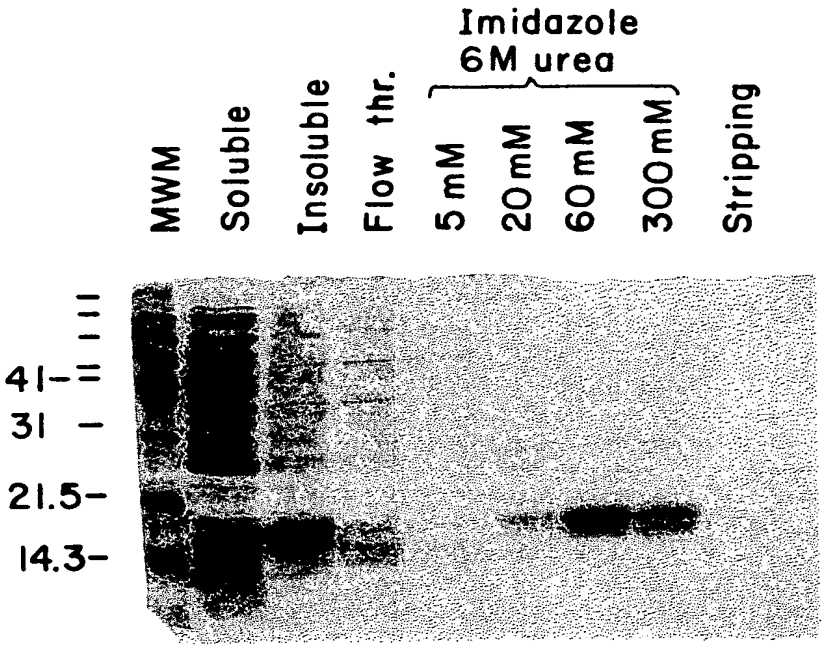


FIG. 18A

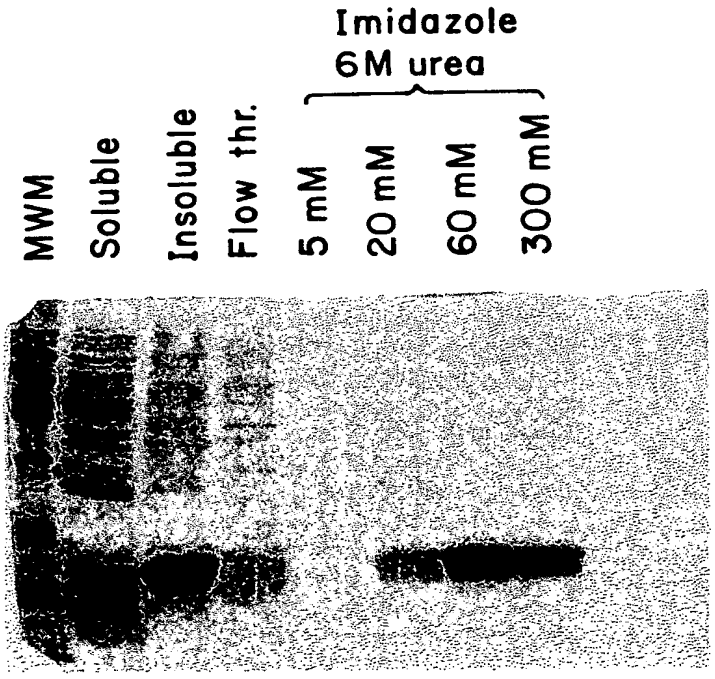


FIG. 18B

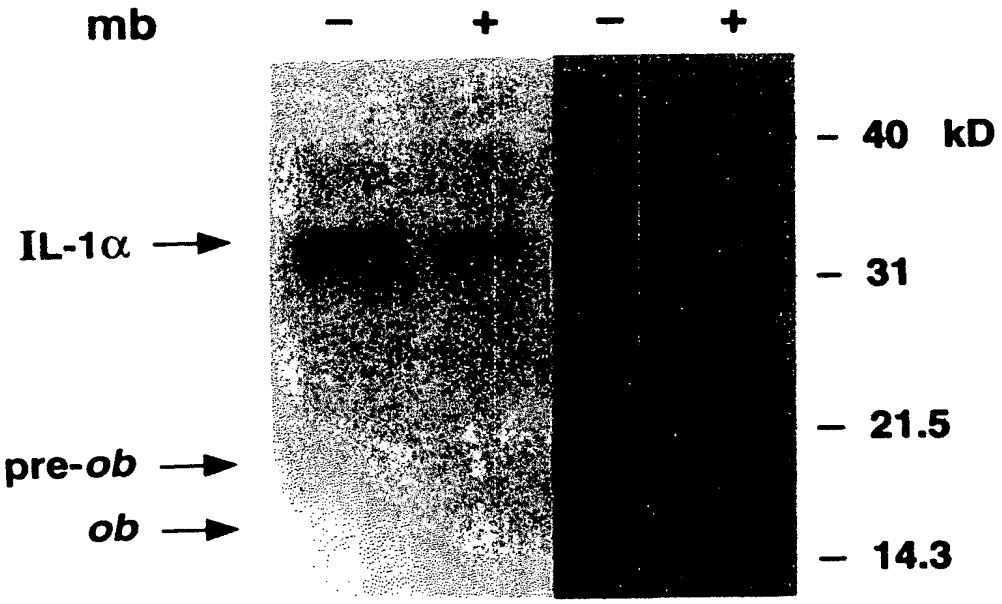


FIG.19A

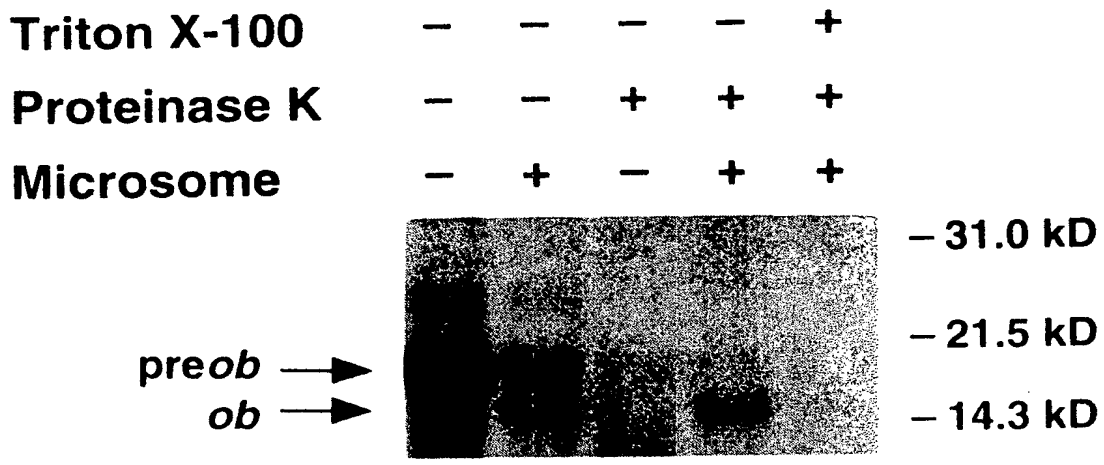


FIG.19B

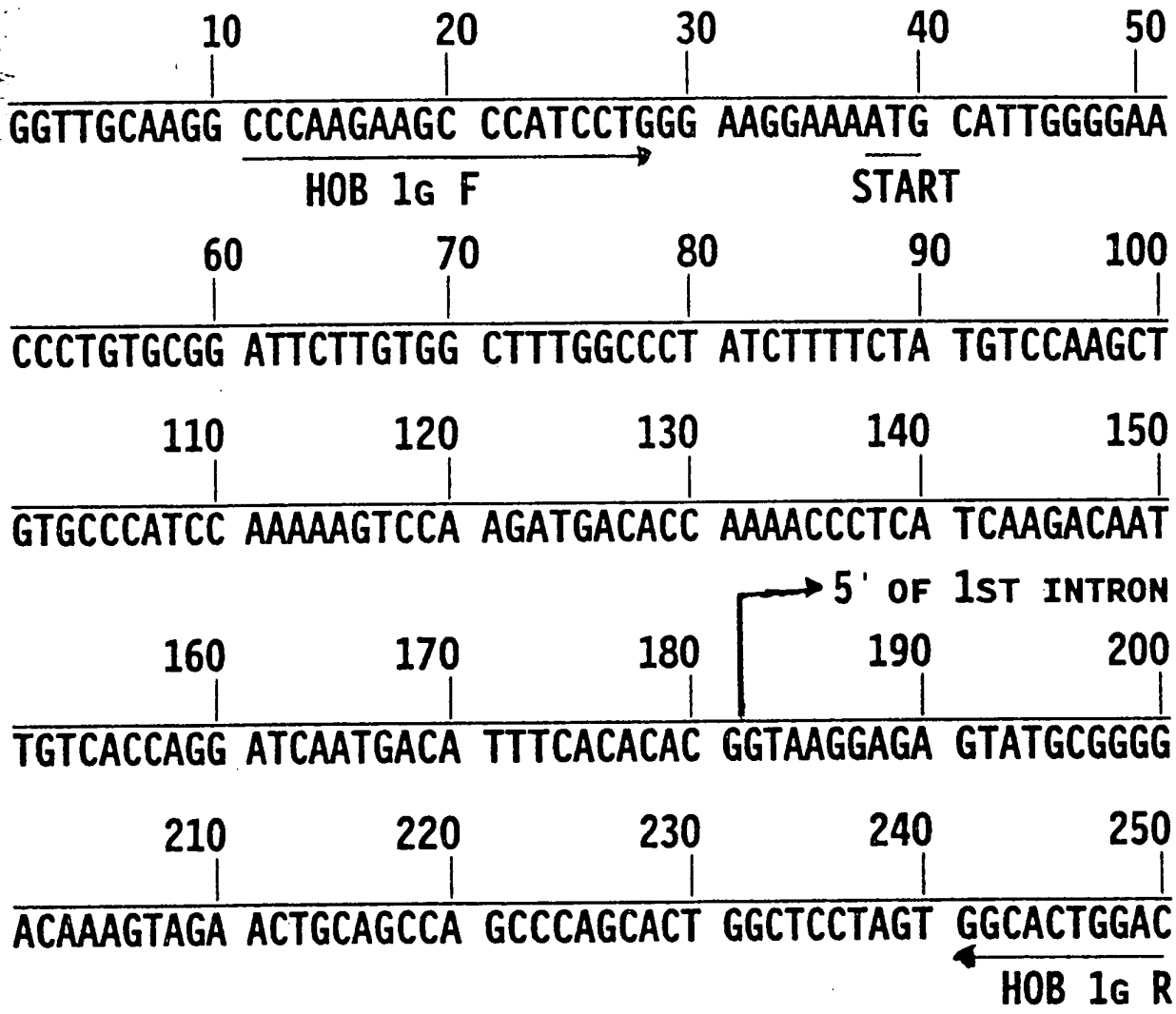


FIG.20A

260 270 280 290 300

CCAGATAGTC CAAGAAACAT TTATTGAACG CCTCCTGAAT GCCAGGCACC

310 320 330 340 350

TACTGGAAGC TGAGAAGGAT TTTGGATAGC ACAGGGCTCC ACTCTTTCTG

360 370 380 390 400

GTTGTTTCTT NTGGCCCCCT CTGCCTGCTG AGATNCCAGG GGTTAGNGGT

410 420 430 440 450

TCTTAATTCC TAAA------ ---------- ---------- --------CT

GAP OF SEQUENCE (~1.4 KB)

460 470 480 490 500

GGTTCTTTCA GGAAGAGGCC ATGTAAGAGA AAGGAATTGA CCTAGGGAAA

FIG.20A-1

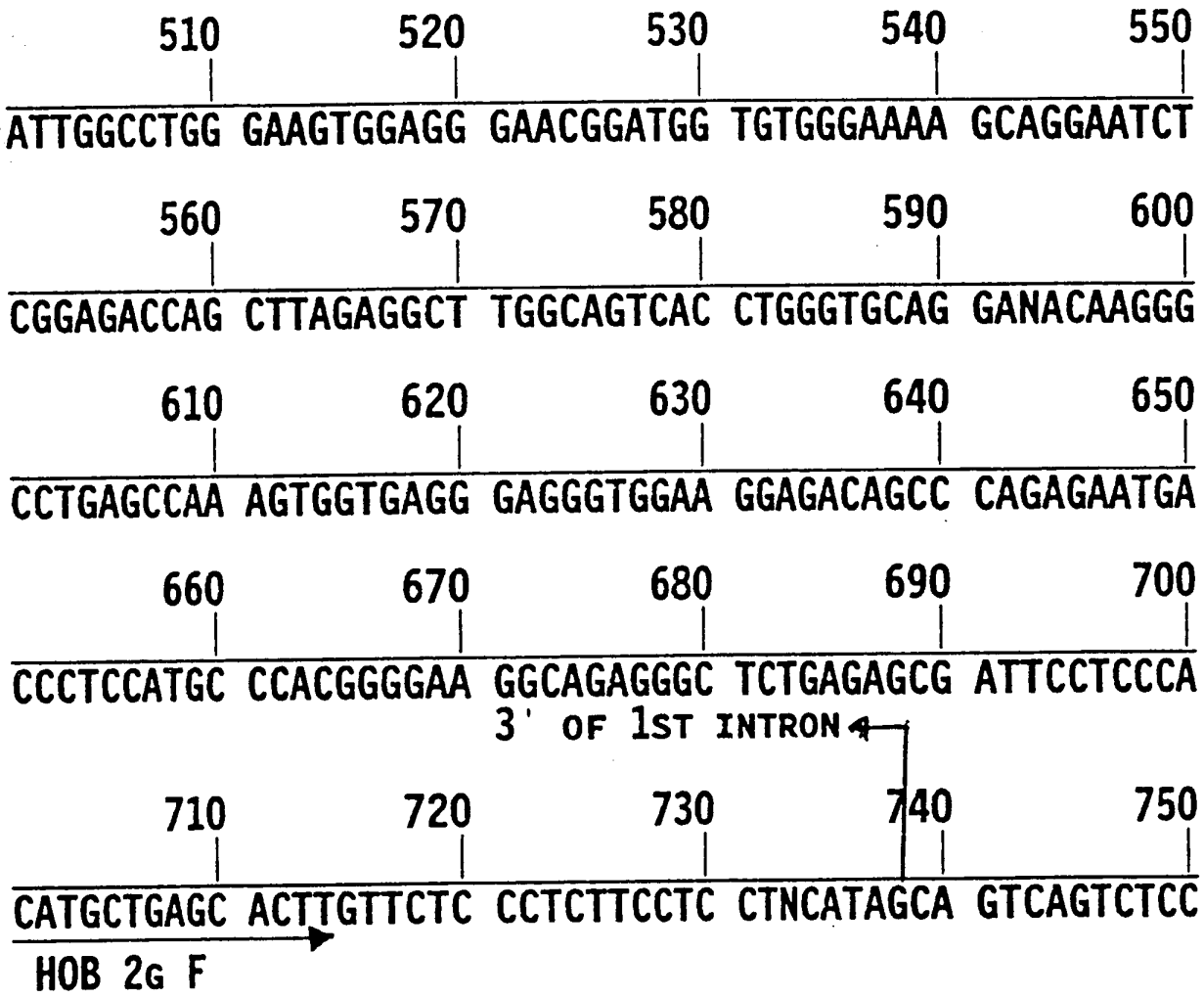


FIG.20A-2

760 770 780 790 800

TCCAAACAGA AAGTCACCGG TTTGGACTTC ATTCCTGGGC TCCACCCCAT

810 820 830 840 850

CCTGACCTTA TCCAAGATGG ACCAGACACT GGCAGTCTAC CAACAGATCC

860 870 880 890 900

TCACCAGTAT GCCTTCCAGA AACGTGATCC AAATATCCAA CGACCTGGAG

910 920 930 940 950

AACCTCCGGG ATCTTCTTCA CGTGCTGGCC TTCTCTAAGA GCTGCCACTT

960 970 980 990 1000

GCCCTGGGCC AGTGGCCTGG AGACCTTGGA CAGCCTGGGG GGTGTCCTGG

FIG.20A-3

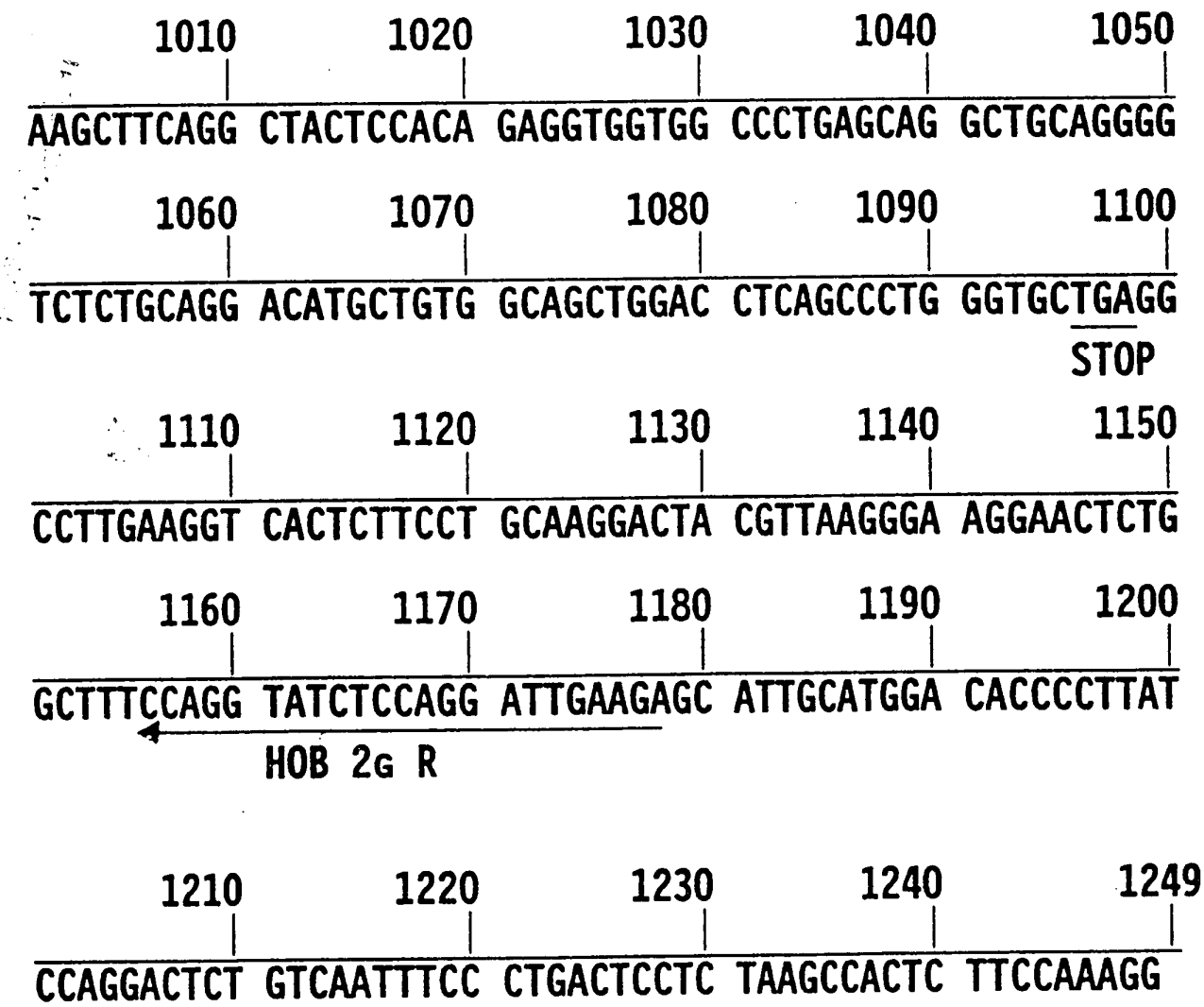


FIG.20A-4

MOUSE OB STRUCTURE

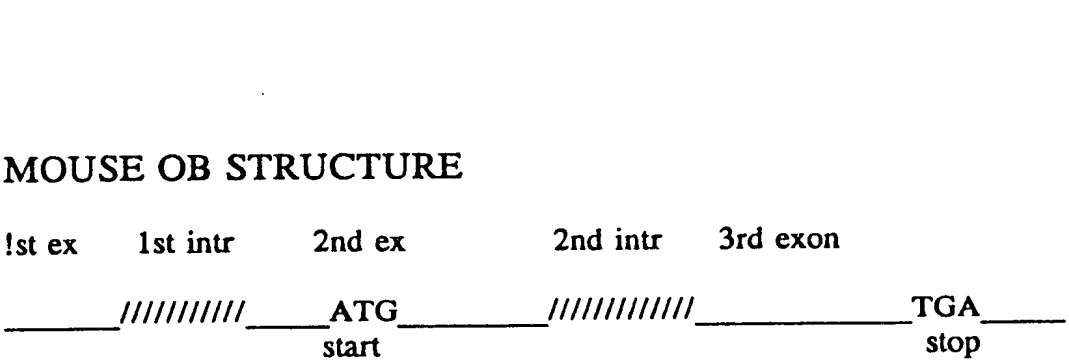


FIG.20B

HUMAN OB STRUCTURE

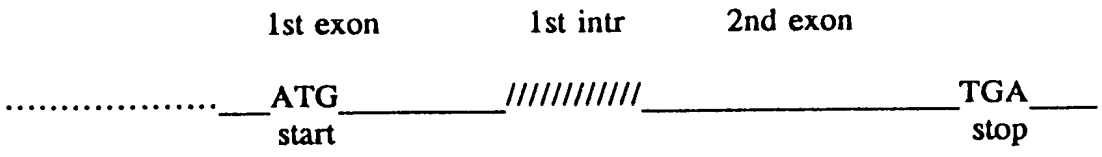


FIG.20C

FIG.21A

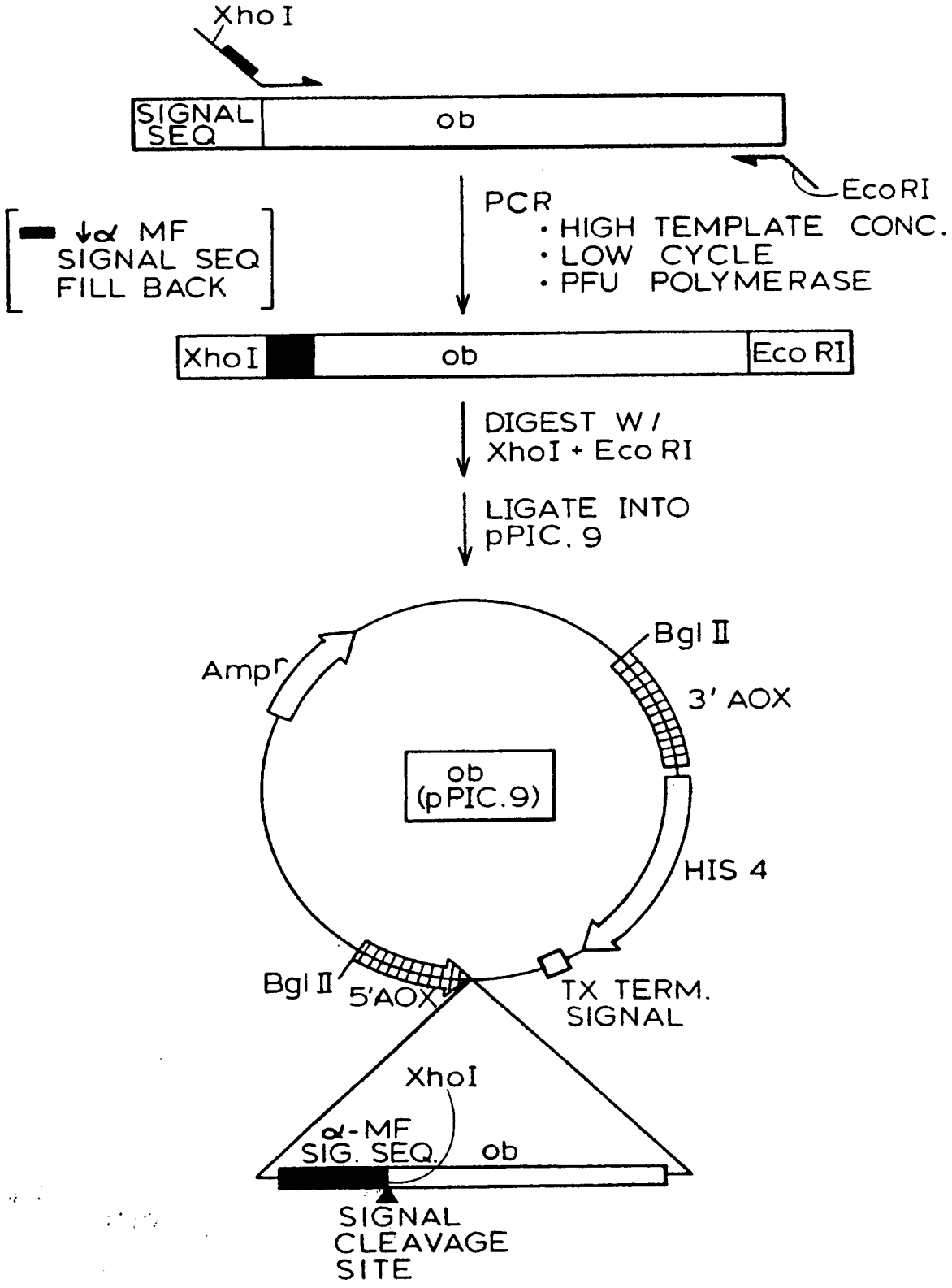


FIG.21B

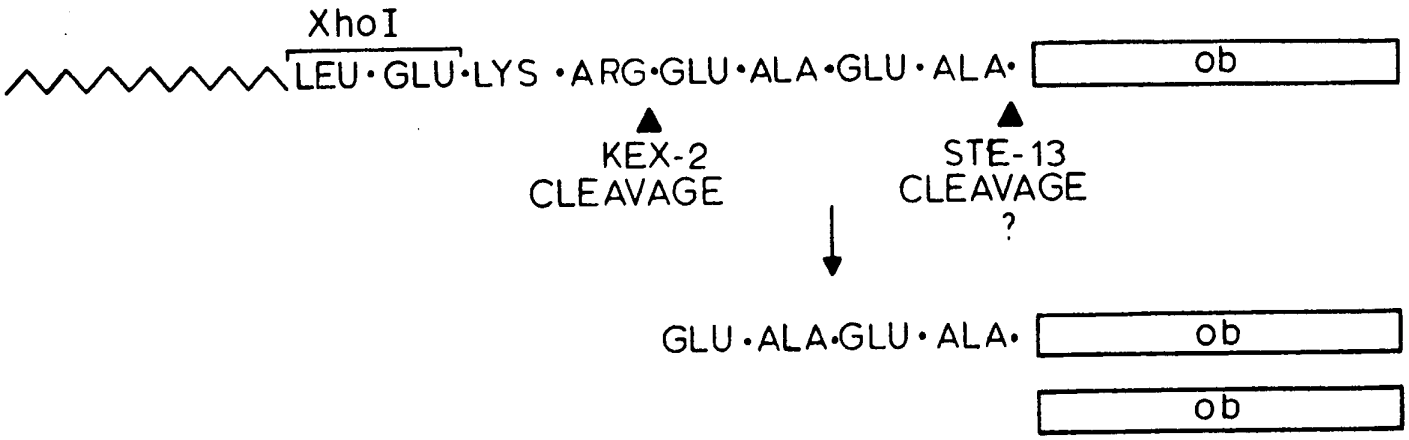


FIG.21C

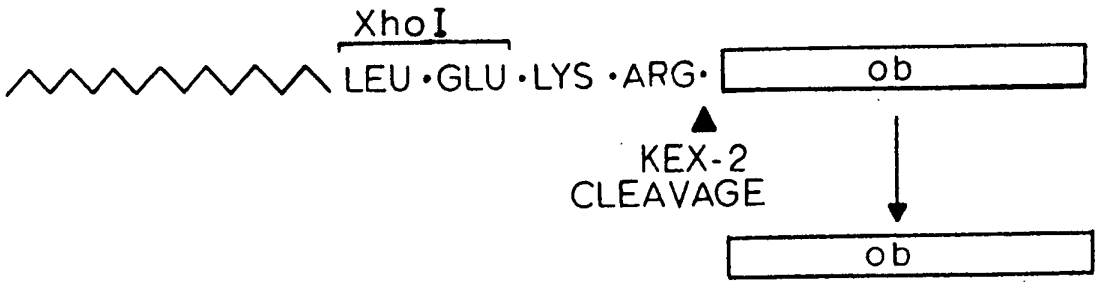
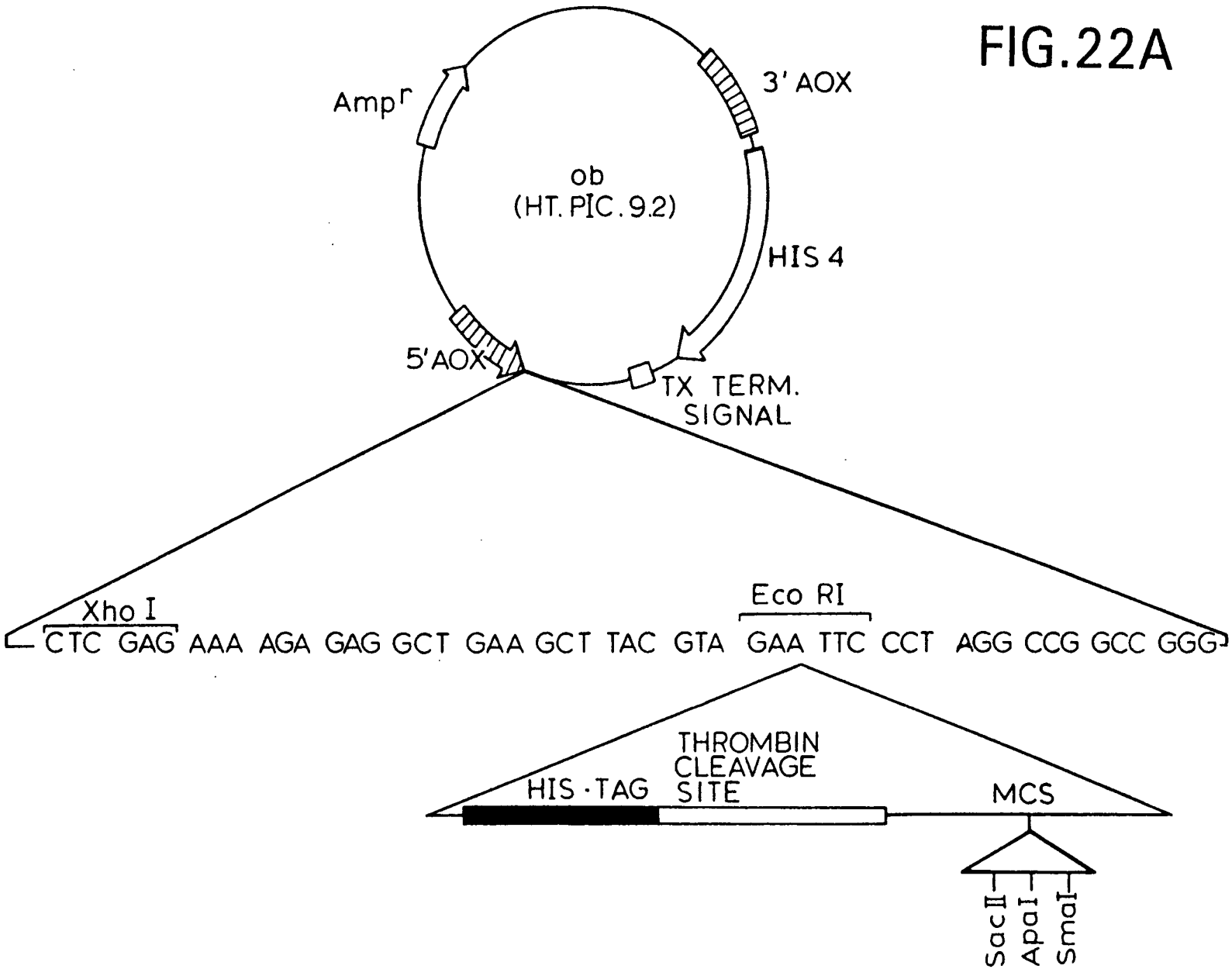


FIG.22A



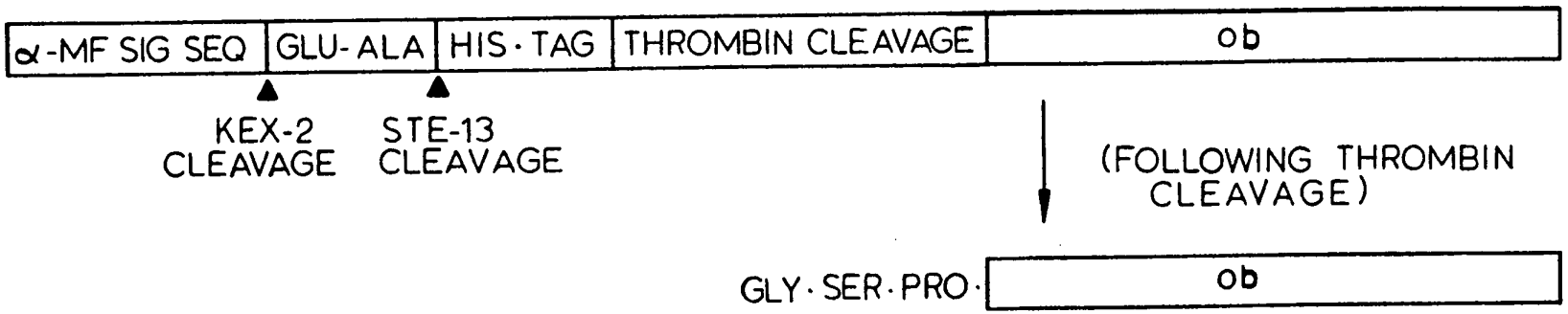


FIG.22B

FIG.23A

1 2 3 4 5

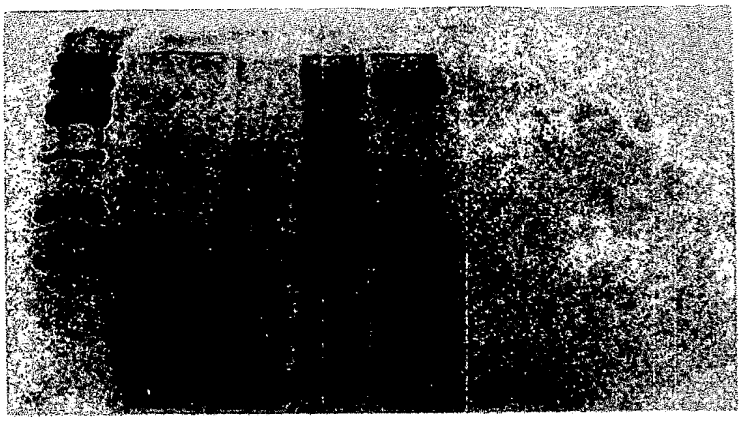


FIG.23B